Center for Surveillance, Epidemiology, and Laboratory Services

Clinical Laboratory Improvement Advisory Committee FDA White Oak Campus Tuesday, April 10, 2018

Implementation of Next-Generation Sequencing in Clinical and Public Health Laboratories

Background/Introduction

Ira M. Lubin, PhD, FACMG
Geneticist
Quality and Safety Systems Branch



Implementation of Next Generation Sequencing in Clinical Laboratories

Background / Introduction

Ira M. Lubin, PhD, FACMG

Public Health Perspective

- Rebecca Hutchins, MS, MBA
- Clinical Laboratory Perspective
- John D. Pfeifer, MD, PhD

CLIAC Discussion

Background / Introduction

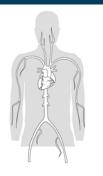
- Next-generation sequencing in clinical and public health applications
- Integrating next-generation sequencing into clinical laboratory testing
- Practice and regulatory framework for assuring the quality of clinical next-generation sequencing
- Proposed CLIAC Workgroup
- Questions for CLIAC

Next-Generation Sequencing in Clinical and Public Health Applications

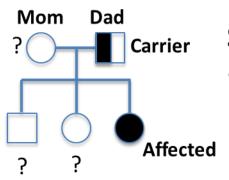


Pediatrics:

- Rare Disease
- Developmental Disabilities

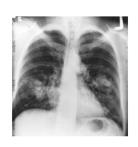


Chronic Disease



Screening:

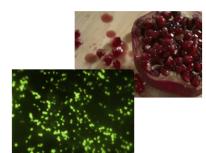
Carrier Screening



Cancer



Transplant



Pathogens:

- Identification
- Outbreak response
- Antibiotic resistance

What is the Landscape of Next-Generation Sequencing Offerings in the United States?

New York Clinical Laboratory Evaluation Program

https://www.wadsworth.org/regulatory/clep/approved-ldt

81 Laboratories

(searched 3/23/2018)

College of American Pathologists Accreditation Data (per organizational contact)

331 laboratories

(provided 3/16/2018)

Genetic Testing Registry

https://www.ncbi.nlm.nih.gov/gtr/

80 Laboratories

(Provided 3/12/2018)

Workflow: Next Generation Sequencing

Indication for testing

Test selection

Specimen and patient data collection

Test order

Clinical setting

1 Patient specimen

Sample Preparation

Instrument Sequencing

Laboratory setting

2 Electronic sample

Discard low quality sequence reads

Alignment/
de novo assembly

Variant calling/ Pathogen ID

Laboratory interpretation

Reporting

Lab result

Test result received

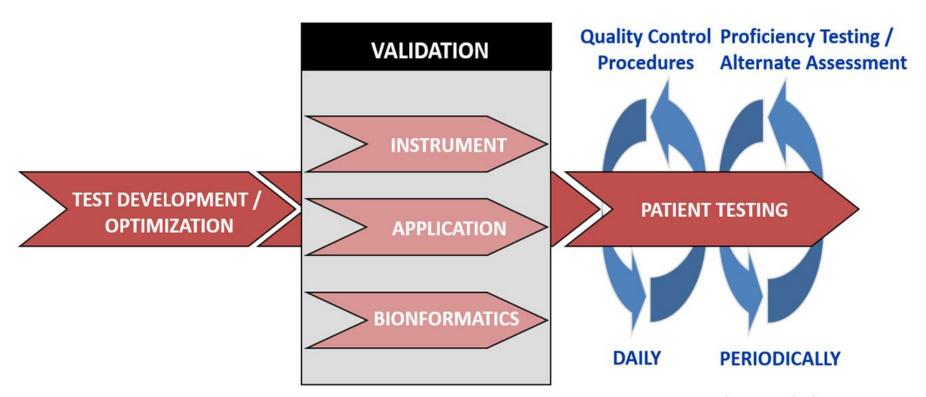
Clinical Interpretation

Application to patient care

Clinical setting

Framework for the Implementation of Clinical NGS Testing

As of 2018, the majority of clinical NGS tests are developed within the laboratory that they are offered.



Gargis et al., Nat Biotechnol. 2012;30:1033

7

Practice and Regulatory Framework for Assuring the Quality of Clinical Next-Generation Sequencing

Applying the CLIA regulations to clinical next-generation sequencing is challenging due to the novelty and complexity of the technology, and new paradigms for data analyses

- Code of Federal Regulations. The Clinical Laboratory
 Improvement Amendments (CLIA). 42 CFR Part 493 sec. 1256.
- Interpretive guidelines: https://www.cms.gov/Regulations-and-Guidance/Guidance/Manuals/Downloads/som107apclab.pdf

Applying CLIA to Next-Generation Sequencing in the Clinical Setting

- Test validation (CLIA general requirements at §493.1253)
- Quality control procedures (CLIA general requirements at §493.1256; unidirectional workflow for molecular amplification at §493.1101 (a)(3))
 - Quality control materials (physical and electronic)?
 - Use of external data to support analyses?
- Test ordering (CLIA general requirements at §493.1241)
- Result Reporting (CLIA general requirements at §493.1291)
- Proficiency testing (CLIA does not specify PT requirements for NGS, so alternative performance assessment requirements at §493.1236(c) apply)
- Personnel competencies (Subpart M; No specific requirements)
- Bioinformatics pipeline quality assessment (No specific requirements)

Other issues:

- Distributive testing single test / multiple sites
- Reporting of secondary findings

Reanalysis

Next Generation Sequencing: Standardization of Clinical Testing

Assuring the quality of next-generation sequencing in clinical laboratory practice

We direct your readers' attention to the principles and guidelines (Supplementary Guidelines) developed by the Nextgeneration Sequencing: Standardization of Clinical Testing (Nex-StoCT) workgroup. These guidelines represent initial steps to ensure that results from tests based on nextgeneration sequencing (NGS) are reliable and useful for clinical decision making. The US Centers for Disease Control and Prevention (CDC) convened this national workgroup, which collaborated to define platform-independent approaches for establishing technical process elements of a quality management system (OMS) to assure the analytical validity and compliance of NGS tests with existing regulatory and professional quality standards. The workgroup identified and addressed gaps in

are summarized in Table 1. Although the workgroup focused on detection of DNA sequence variations associated with heritable human disorders, many of the principles and recommendations described are also relevant to the application of NGS to other areas of laboratory medicine, including the diagnosis, prognosis and

Document reli-

platform, test,

Requirements for

Gargis et. al. Nat. Biotechnol. 2012;

30:1033-1036+ Supplemental

test establishment. Objective

treatment of cancer and infectious, disease

Validation is the process of establishing analytical performance specifications for a clinical test system developed in house to confirm that the system is suitable for its intended use1. During the validation process, the laboratory must demonstrate that the assay functions as expected and provides

•Platform validation: establish that the system pro sequence analysis across the genomic regions to •Test validation: establish that the system correct genome (Supplementary Guidelines, section 4). testing of patient •Informatics pipeline validation: establish that the reliably analyze platform data to produce an ac

Principles and Recommendations for Standardizing the Use of the Next-Generation Sequencing Variant File in Clinical Settings

Ira M. Lubin, * Nazneen Aziz, Lawrence J. Babb, Dennis Ballinger, Himani Bisht, Deanna M. Church, ** Shaun Cordes, Dennis Ballinger, Himani Bisht, Deanna M. Church, ** Shaun Cordes, Dennis Ballinger, Himani Bisht, Deanna M. Church, ** Shaun Cordes, Dennis Ballinger, Dennis Ballinge Karen Eilbeck, Fiona Hyland, Lisa Kalman, Melissa Landrum, Edward R. Lockhart, Donna Maglott, Gabor Marth, John D. Pfeifer, Heidi L. Rehm, *** Somak Roy, Zivana Tezak, Rebecca Truty, Mollie Ullman-Cullere, Karl V. Voelkerding, 555 Elizabeth Worthey, 555 Alexander W. Zaranek, and Justin M. Zook

Good laboratory practice for clinical next-generation sequencing informatics pipelines

To the Editor:

We report principles and guidelines (Supplementary Note) that were developed by the Next-Generation Sequencing: Standardization of Clinical Testing II (Nex-StoCT II) informatics workgroup, which was first convened on October 11-12, 2012, in Atlanta, Georgia, by the US Centers for Disease Control and Prevention (CDC; Atlanta, GA). We present

recommendations are summarized in Table 1, and detailed in the guidelines presented in the Supplementary Note.

Currently, most clinical NGS tests are offered as laboratory-developed tests (LDTs), which are tests designed, manufactured and used within a single laboratory. These tests use commercially available sequencing platforms to generate raw sequence data that are subsequently

Lubin IM et al. I Mol Diagn. 2017;19:417-426

Gargis et al. Nat. Biotechnol.

CDC facilitated the development of the first consensus guideline for clinical next-generation sequencing.

2015;33: 689-693 + Supplemental

The Food and Drug Administration: Draft Guidance for Next-Generation Sequencing

Contains Nonbinding Recommendations

Draft - Not for Implementation

Infectious Disease Next Generation Sequencing Based Diagnostic Devices: Microbial Identification and Detection of Antimicrobial Resistance and Virulence Markers

Draft Guidance for Industry and ¹ Food and Drug Administration Staff ²

DRAFT GUIDANCE

This draft guidance document is being distributed for comment purposes only.

13

Document issued on: May 13, 2016

Contains Nonbinding Recommendations Draft - Not For Implementation

Use of Standards in FDA Regulatory Oversight of Next Generation Sequencing (NGS)-Based In Vitro Diagnostics (IVDs) Used for Diagnosing Germline Diseases

Draft Guidance for Stakeholders and Food and Drug Administration Staff

DRAFT GUIDANCE

This draft guidance document is being distributed for comment purposes only.

Document issued on July 8, 2016.

You should submit comments and suggestions regarding this draft document within 90 days of

15

Contains Nonbinding Recommendations Draft - Not For Implementation

Use of Public Human Genetic Variant Databases to Support Clinical Validity for Next Generation Sequencing (NGS)-Based In Vitro Diagnostics

Draft Guidance for Stakeholders and Food and Drug Administration Staff

DRAFT GUIDANCE

This draft guidance document is being distributed for comment purposes only.

Document issued on July 8, 2016.

You should submit comments and suggestions regarding this draft document within 90 days of publication in the Federal Register of the notice announcing the availability of the draft guidance. Submit electronic comments to http://www.regulations.gov. Submit written

A Sampling of Professional Guidance



MM09-A2

Nucleic Acid Sequencing Methods in Diagnostic Laboratory Medicine: Approved Guideline—Second Edition

ACMG PRACTICE GUIDELINES

ACMG clinical laboratory standards for next-generation sequencing

Heidi L. Rehm, PhD^{1,2}, Sherri J. Bale, PhD², Pinar Bayrak-Toydemir, MD, PhD⁴, Jonathan S. Berg, MD⁵, Kerry K. Brown, PhD⁴, Joshua L. Deignan, PhD³, Michael J. Friez, PhD⁸, Birgit H. Funke, PhD^{1,2} Madhuri R. Hegde, PhD⁹ and Elaine Lyon, PhD⁶; for the Working Group of the American College of Medical Genetics and Genomics Laboratory Quality Assurance Committee

finical laboratory geneticists to help them provide quali not necessarily assure a successful reedical outcome. T he clinical laboratory geneticist should apply his or her

Next-generation sequencing technologies have be be deployed in clinical laboratories, enabling raj in genomic medicine. These technologies have large-scale sequencing by several orders of magn our advances are being made. It is now feasible vidual's near-complete exome or genome to ass of a wide array of clinical scenarios. Next-gen

standard. However, its limitations include for high cost, making multigene panels laborior

Objective.—To develop a checklist for clinical testing Recent technological advancements have radi using NGS technology that sets standards for the analytic landscape of medical sequencing. Next-gen

College of American Pathologists' Laboratory Standards

CAP Laboratory Improvement Programs

for Next-Generation Sequencing Clinical Tests Nazneen Aziz, PhD; Qin Zhuo, PhD; Lynn Bry, MD, PhD; Denise K. Driscoll, MS, MT/ASCP/SBB; Birgit Funke, PhD; Jane S. Cibson, PhD; Wayne W. Crody, MD; Madhuri R. Hegde, PhD; Gerald A. Hoelge, MD; Debra G. B. Leonard, MD, PhD; Jason D. Merker, MD, PhD; Rakesh Nagarajan, MD, PhD; Linda A. Palicki, MT(ASCP); Ryan S. Robetorye, MD; Iris Schrijver, MD; Karen E. Weck, MD; Karl V. Voelkenling, MD

· Context.—The higher throughput and lower per-base cost of next-generation sequencing (NGS) as compared to Sanger sequencing has led to its rapid adoption in clinical testing. The number of laboratories offering NGS-based A. INTRODUCTION
Lests has also grown considerably in the past few years, sequencing technologies have evolved rapid despite the fact that specific Clinical Laboratory Improveyears, Semi-automated Sanger sequencing 1 ment Amendments of 1988/College of American Patholoclinical testing for many years and is still co gists (CAP) laboratory standards had not yet been

in (NGS) technologies utilize density am miscoel templates, which are then sequen-magnitude. NGS technologies are now being chinical settings. Three main levels of analyst technologies are now being chinical settings. Three main levels of analyst technologies are nown inclusions. The second of the control of the control of the control of the Victorian is ablacted before the newn inclusions con-trol of the control of the Victorian is beginned to the control of the control of the control of the Victorian is beginned to the control of the co

wet bench process and for bioinformatics or "dry bench" analyses. As NGS-based clinical tests are new to diagnostic testing and are of much greater complexity than traditional Sanger sequencing-based tests, there is an urgent need to develop new regulatory standards for laboratories offering

Design.—To develop the necessary regulatory frame-work for NGS and to facilitate appropriate adoption of this technology for clinical testing, CAP formed a committee in

technology for clinical lessing, CAP formed a committee in 2011, the NGS Work Group, to deliberate upon the contents to be included in the checklist. Results—A total of 11 laboratory accreditation checklist requirements for the analytic wet bench process and bioinformatics analysis processes have been included within CAP's molecular pathology checklist MODI. Conclusions.—This report describes the important issues-

considered by the CAP committee during the development of the new checklist requirements, which address documen-tation, validation, quality assurance, confirmatory testing, exception logs, monitoring of upgrades, variant interpreta-tion and reporting, incidental findings, data storage, version traceability, and data transfer confidentiality. (Arch Pathol Lab Med. 2015;139:481–493; doi: 10.5858/ arpa.2014-0250-CP)

DNA sequencing has evolved from Maxam-Gilbert¹ and Sanger¹³ methods in the 1970s to a set of technologies that are collectively referred to an experimental set.

SPECIAL ARTICLE

July 2, 2015.

Benjamin A. Placky, M.D.

Ph.D. Department of Pathol-ogs, Stanford University School of Medicine, 3375 Hilbstew Ave. Room 2913, Palo

Alto, CA 94001, E-mail

Next-Generation Sequencing for Infectious

Martina I. Lefterova, "T Carlos J. Suarez, "T Niaz Banaei, "T and Benjamin A, Pinsky"

ONE Assemblation Statement: This activity ("DMD 2015 CME Program in Michaelle Discounted") has been showed and involve in of the Accrelitation Council for Continuing Medical Education (ACCME) through the joint providership of the American Society for Cli-from Society for Investigative Pethology (ASEP). ASCP is accredited by the ACCME to provide continuing medical education for physician

CME Disclosures: The authors of this article and the planning committee members and staff have no Minster Strancial relation

Disease Diagnosis and Management

Guidelines for diagnostic next-generation sequencing

Gert Matthijs*,1,8, Erika Souche1,8, Mariëlle Alders2, Anniek Corveleyn1, Sebastian Eck3, Ilse Feenstra4, Valérie Race¹, Erik Sistermans⁵, Marc Sturm⁶, Marjan Weiss⁵, Helger Yntema⁴, Egbert Bakker⁷, Hans Scheffer⁴ and Peter Baum⁶

We present, on behalf of EuroGentest and the European Society of Human Genetics, guidelines for the evaluation and validation we present, on bothal of Eurodesides' and the European Society of Hard Interaction, placeholises for the evaluation and validation of order agreements or expensively. Biological prices for the first ground of present describes, this was as performed by a purpose of order datashcides in the field of human genetics. The statements that new widths during the situations of the galacties are presented here. The background document and flat galacties are washile as supplementary material. They include many examples to avail the blootstries in the implementation of NGC and accrossition of this service, The work and ideas presented by others in publishes that these energies developed the content of the placeholises are developed to the publishes and the publishes are shall be as supplementary material. They include many examples to available as supplementary instantial, they include many examples to available that the presented excellent in the content of the post they many weath considered and other placeholises are presented by others in publishes that have energied excellent in the content of the post they many weath considered and publishes are supplementation of the publishes are weather than the content of the post they many weath considered and publishes are publishes as the publishes are published to the publishes and the publishes are published to the publishes and the publishes are published to the pu acknowledged in the full text. Interestingly, a few new insights that have not been cited before have emerged during the acknowledges in the faul text interestingly, a line even integral that have not been close device have energies during the preparation of the glorideries. The noted important new feature is the presentation of a "artiting system" for MSO-based diagnostic tests. The guidelines and statements have been applicated by the genetic diagnostic community, and thus seem to be valuable for the harmonication and quality assurance of MSO diagnostics in Europe.

European Journal of Human Genetics (2016) 24, 2-6; doi:10.1038/pig.2015-226; published online 28 October 2015

thousands to millions of low pain of DNs superace of an individual in hydrogene of the paint. The relabely fast emergance and the gross secons of the paint and paint. The relabely fast emergance and the gross secons of the paint and the pai reduction to the or exclusing the rings, whentigh which if the trivials of the control of the co machines and shift for performing NOS in diagnosis, must insent here to be don't bit. It is in this content that we propose the guidelines. These guidelines mustly dud with NOS tortig in the content of are and mostly managain cleanes. The mainly focus our content of are and mostly managain cleanes. The mainly focus or explicit of the fall reviews of the guidelines and explored in the layer. They are more extensively explored in the fall reviews of the guidelines, market are explosed in the fall reviews of the guidelines, market are explosed in the fall reviews of the guidelines, market are supplementary market districts, and assept, or by extracting data from white-coarse expension, in

sporncing would also

-d shortly will - also practical examples and templates.

Next Generation Sequencing **Implementation** Guide



APHL ASSOCIATION OF

NEW YORK | Department of Health

Best practices for evaluating single nucleotide variant calling methods for microbial genomics

including automation, standardizing technical protocols and bioinformatics pipe

Nathan D. Olson 1*, Steven P. Lund 2, Rebecca E. Colman 3, Jeffrey T. Foster 41, Jason W. Sahl 34, James M. Schupp 3, Paul Keim 34, Javne B. Morrow 1, Marc L. Salit 1,5 and Justin M. Zook SPECIAL ARTICLE

HOWARD A. ZUCKER, M.D., J.D. SALLY DRESLIN, M.S., R.N.

Scoystoms and Biomaterials Division, Material Measurement La

Roughment and someone in control represents Debtor, Information and Engineering Debtor, Information and Engineering Debtor, Information and Enchrology, Guittenburg, MCJ. USA, **Debtor of Pathogon Guidelines for Validation of Next-Generation USA *Department of Bioengineering, Stantord University, Stanto Sequencing—Based Oncology Panels

Innovations in sequencing technologies hav A Joint Consensus Recommendation of the Association for advances in understanding biological syste increasingly recognize that analyzing the v Molecular Pathology and College of American Pathologists

> *1 Christopher Corless, *1 Suzanne Kamel-Reid, *11 Ira M. Lubin, *** John Pfeifer, *11 and Marina N. Nikiforova*

> hildren's Hospital of Chicago, Norshwestern University's Feinberg School of Medicine, Chicago, Illinois w York. New York: the Denartment of Pathology and Knight Concer Institute. Occors Health and Science we core, sees 10st, not Expansions of cosmology and English Lancer sources. Origin trains and science Clinical Laboratory Genetics, University Health Network, Toronto, Ontario, Canada; the Department of service of Toronto, Toronto, Origin, Canada; the Centers for Disease Control and Prevention, ** Allento,

UPDATED AND REVISED

March 2016

Executive Deputy Commissione

Oncology - Molecular and Cellular Tumor Markers

"Next Generation" Sequencing (NGS) guidelines for somatic genetic variant detection

The following describes requirements for the development of procedures and the establishment of performance (validation) of assays for the detection of somatic genetic variants by Next



12

Summary

- Next generation sequencing is continuing to integrate into diverse medical disciplines.
- Bioinformatics (computational analysis) comprises a significant component of the test.
- Communication between the laboratory professional (s) and clinician(s) is vital toward understanding of the available testing, limitations, and test findings
- Clinical NGS testing is covered under CLIA but application of the laboratory requirements may not be sufficiently defined.

Proposed CLIAC NGS Workgroup

Proposed Charge

Provide input to CLIAC for consideration in developing recommendations to CDC, CMS, and FDA for assuring the quality of next generation sequencing in clinical laboratory settings

Proposed Workgroup Tasks

- Identify challenges in applying the existing regulatory framework
- Identify challenges and gaps in guidance
- Consider and suggest strategies to address the identified gaps and challenges
- Consider and suggest strategies for assuring workforce competency

Questions for CLIAC

- 1. What major gaps and issues do laboratories experience when implementing NGS-based testing for various applications?
- 2. What guidance is lacking for laboratories that perform NGS testing to address critical steps in the total testing process?
- 3. How can CDC, CMS, and FDA assist in filling NGS-related gaps and providing guidance to laboratories?



Ira M. Lubin, PhD, FACMG <u>ilubin@cdc.gov</u>

For more information please contact Centers for Disease Control and Prevention

1600 Clifton Road NE, Atlanta, GA 30333

Telephone: 1-800-CDC-INFO (232-4636)/TTY: 1-888-232-6348

E-mail: cdcinfo@cdc.gov | Web: www.cdc.gov

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.